

B1 or the primer annealing sequences of the original wild-type template. The mutated template amplifies with equal efficiency as the wild type template in a number of TCRBV-specific PCR reactions. See Higuchi R., et al (1988) *Nucleic Acids Res.* 15, 7351-7367 and Ho S.N., et al (1989) *Gene* 77, 51-9, for further details on gene SOEing.

On page 36, please replace the first complete paragraph with the following, amended and clean paragraph:

B2 Alternatively, as the TCRBJ segments BJ1S1, BJ2S1 and BJ2S7 seem to be the most frequently used, measuring the TCRBV-BJ combinations for just these three segments will approximate to 40-45% of the total V β -specific T cell gene rearrangements for most V β s [Jeddi-Tehrani et al (1994) *Human Immunology* 40, 93-100]. Quantitation of TCRA mRNA, total and specific, may also be achieved using the RT-CPCR method. In the first instance, TCRA mutants have to be manufactured. In the reverse of the TCRB method, mutants have the SEQ ID NO: 2 (GATGTCAAGCTGGTCGAGAA) wild-type TCRAC sequence replaced with the equivalent sequence from the TCRBC chain, SEQ ID NO: 1 (CATCAGAAGCAGAGATCTCC) by gene SOEing. This may be performed to sequences derived using TCRAV- and TCRAC-specific primers (for quantification of specific α chain message) or in sequences amplified using two TCRAC-specific primers (for quantitation of total $\alpha\beta$ mRNA).

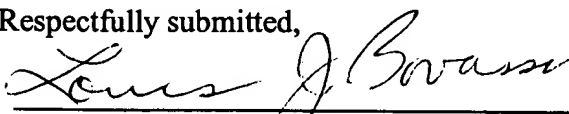
REMARKS

Applicant, through undersigned counsel, wishes to thank the Examiner for the careful examination as to the formalities of the application. Applicant respectfully request entry of this amendment.

Please charge any additional fees or credit overpayment to Deposit Account No. 16-2230.

Dated: March 5, 2002.

Respectfully submitted,



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